Claims: -

1. A method for identifying a gene having a role in the presentation of diabetic nephropathy, which method comprises culturing mesangial cells in a medium in the presence of a concentration of glucose sufficient to induce differential expression of a gene susceptible to such differential expression and identifying the gene so induced by suppression subtractive hybridisation.

2. A method according to Claim 1, wherein the mesangial cells are cultured in the presence of a concentration of glucose sufficient to induce up-regulation of a gene susceptible to such up-regulation.

3. A method according to Claim 1 or 2, wherein the concentration of glucose is greater than 5 mM.

4. A method according to any preceding claim, wherein the mesangial cells are subjected to mechanical strain.

5. A method according to any preceding claim, wherein transforming growth factor β1 (TGF-β1) is added to the culture medium.

6. A method according to any one of Claims 1-5, wherein the possibility of differential expression due to hyperosmolarity is excluded.

7. A method according to any one of Claims 1-6, wherein the gene so differentially expressed is a gene which includes a sequence selected from:

1) SEQ ID NOS: 1-3;

2) SEQ ID NO: 4;

3) SEQ ID NO: 5; and

4) SEQ ID NO: 6.

8. Use of a gene identified by a method according to any one of Claims 1-7, as a diagnostic marker for the progression and presentation of diabetic nephropathy.

9. Use of a gene identified by a method according to any of Claims 1-7, as an index of disease activity and the rate of progression of diabetic nephropathy.

10. Use of a gene identified by a method according to any of Claims 1-7, as a basis for identifying drugs for use in the prevention and/or therapy of diabetic nephropathy.

11. A sequence selected from any one of SEQ ID NOS: 1-3, 5 and 6 according to Claim 7.

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